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Citing IMGT/V-QUEST:

Brochet, X. et al., Nucl. Acids Res. 36, W503-508 (2008). [PMID: 18503082](#). [PDF](#)

Giudicelli, V., Brochet, X., Lefranc, M.-P., Cold Spring Harb Protoc. 2011 Jun 1;2011(6). pii: pdb.prot5633. doi: 10.1101/pdb.prot5633.

[PMID: 21632778](#) [Abstract](#) also in *IMGT booklet with generous provision from Cold Spring Harbor (CSH) Protocols* [PDF](#) (high res). [PDF](#) (lower res)

IMGT/V-QUEST program version: [3.5.24](#) (9 March 2021) - IMGT/V-QUEST reference directory release: [202113-2](#) (30 March 2021)

Species	Homo sapiens (human)
Receptor type or locus	IGL
IMGT directory reference set	F+ORF+ in-frame P
Search for insertions and deletions	no

A. Detailed results for the IMGT/V-QUEST analysed sequences

Number of analysed sequences: **1**

1. [9](#)

Hyphens (-) show nucleotide identity, dots (.) represent gaps

Sequence: 1 9

Analysed sequence length: 323.

Sequence analysis category: 1 (no indel search).

Sequence compared with the [Homo sapiens \(human\) IGL set](#) from the [IMGT reference directory](#) (set: F+ORF+ in-frame P)

>9

```
acatccagatgacccagtctccatcttccgtgtctgcatctgtaggagacagagtcacca  
tacttgtcggcgagtcagggtattttcagctggttagcctggtatcagcagaaaccag  
gaaaagcccctaagctcctgatctatgctgcttccagtttacaagtggggtcccatcaa  
gattcagcggcagtggtatctgggacagatttcactctcaccatcagcagcctgcagcctg  
aggattttgcaatttactattgtcaacaggctaacagtggtcccgatcaccttcggccaag  
ggacacgactggagattaaacga
```

Result summary: 9

No rearrangement found (a)

Result summary: 9	No rearrangement found (a)		
V-GENE and allele	Homsap IGLV1-40*01 F	score = 225	identity = 53.41% (149/279 nt)
FR-IMGT lengths, CDR-IMGT lengths	[6.3.X]		

(a) Low V-REGION identity (53.41%); the submitted sequence and the closest germline V-GENE allele show different CDR1-IMGT amino acid lengths (6 AA in 9; 9 AA in Homsap_IGLV1-40*01): this may indicate potential nucleotide insertion(s) and/or deletion(s) . Try 'Search for insertions and deletions' in 'Advanced parameters' at the bottom of the Search page

1. Alignment for V-GENE and allele identification

Closest V-REGIONS (evaluated from the V-REGION first nucleotide to the 2nd-CYS codon plus 18 nt of the CDR3-IMGT)

		Score	Identity
M94116	Homsap IGLV1-40*01 F	225	53.41% (149/279 nt)
X53936	Homsap IGLV1-40*02 F	216	53.05% (148/279 nt)
Y12415	Homsap IGLV2-11*03 F	209	53.52% (137/256 nt)
Y12413	Homsap IGLV2-14*04 F	209	53.52% (137/256 nt)
Z22192	Homsap IGLV1-40*03 F	207	52.69% (147/279 nt)
AC279317	Homsap IGLV4-60*03 F	207	52.69% (147/279 nt)
X71966	Homsap IGLV3-21*01 F	198	52.33% (146/279 nt)
D87000	Homsap IGLV4-60*02 F	198	52.33% (146/279 nt)
Y12418	Homsap IGLV2-8*03 F	191	52.73% (135/256 nt)
M30446	Homsap IGLV1-51*02 F	189	51.97% (145/279 nt)

Alignment with [FR-IMGT](#) and [CDR-IMGT](#) delimitations

```

9
M94116 Hom sap IGLV1-40*01 F
X53936 Hom sap IGLV1-40*02 F
Y12415 Hom sap IGLV2-11*03 F
Y12413 Hom sap IGLV2-14*04 F
Z22192 Hom sap IGLV1-40*03 F
AC279317 Hom sap IGLV4-60*03 F
X71966 Hom sap IGLV3-21*01 F
D87000 Hom sap IGLV4-60*02 F
Y12418 Hom sap IGLV2-8*03 F
M30446 Hom sap IGLV1-51*02 F

<----- FR1-IMGT -----
atccagatgaccagctctccatcttcc...gtgtctgcatctgtaggagacagagtcacc
cagtctg--ctgac-cag--gc-c--a...-----ggg-ccc---gc-g--g-----
cagtctg-cgtgac-cag--gc-c--a...-----ggg-ccc---gc-g--g-----
.....C--a...-----C-gg---cct---c-gtc-----
.....C-----gg---cct---c-gtcga-----
cagtctg-cgtgac-cag--gc-c--a...-----ggg-ccc---gc-g--g-----
cag-ctg--ctgactcaat---c--t...-cc-----t--cc-g---tc-tcg---ag
tc-t-tg--ctgactcag---c-c--a...-----a-tgg-ccc---a-g-cg-c--gg
cag-ctg--ctgactcaat---c--t...-cc-----t--cc-g---tc-tcg---ag
.....C-----c---c-gg---cct---c-gtc-----
cagtctg--ttgac-cag--gc-c--a...-----gg-ccc---c-g-ag-----

```

```

9
M94116 Hom sap IGLV1-40*01 F
X53936 Hom sap IGLV1-40*02 F
Y12415 Hom sap IGLV2-11*03 F
Y12413 Hom sap IGLV2-14*04 F
Z22192 Hom sap IGLV1-40*03 F
AC279317 Hom sap IGLV4-60*03 F
X71966 Hom sap IGLV3-21*01 F
D87000 Hom sap IGLV4-60*02 F
Y12418 Hom sap IGLV2-8*03 F
M30446 Hom sap IGLV1-51*02 F

----->_____ CDR1-IMGT _____<-----
atcacttgtcgggcgagtcagggtatt.....ttcagctgggttagcc
---t-c--cact-g--cagctcc-acatcggg.....gcaggttatgatg--ca-
---t-c--cact-g--cagctcc-acatcggg.....gcaggttatgatg--ca-
---t-c--cact-ga-ccagca--ga-gttggt.....ggt-at-a--atg-ct--
---t-c--cact-ga-ccagca--gacgttggt.....ggt-at-a--atg-ct--
---t-c--cact-g--cagctcc-acatcggg.....gcaggttatgatg--ca-
c----c--cactct--cagt--gcacagt.....ag-ta-atca-c--a
--t--c---g---ga-aca-cat-gga.....agt-aaa-tg-gca-
c----c--cactct--cagt--gcacagt.....ag-ta-atca-c--a
---t-c--cact-ga-ccagca--gacgttggt.....ggt-at-a--atg-ct--
---t-c--ctct-ga--cagctcc-acatt.....gggaat-at-atg--t--

```

```

9
M94116 Hom sap IGLV1-40*01 F
X53936 Hom sap IGLV1-40*02 F
Y12415 Hom sap IGLV2-11*03 F
Y12413 Hom sap IGLV2-14*04 F
Z22192 Hom sap IGLV1-40*03 F
AC279317 Hom sap IGLV4-60*03 F
X71966 Hom sap IGLV3-21*01 F

----- FR2-IMGT ----->_____ CDR
tggtatcagcagaaccaggaaaagcccctaagctcctgatctatgctgct.....
----c-----ctt-----c-----c--a----c-----g-aac.....
----c-----ctt-----c-----c--a----c-----g-aac.....
----c--a--ac-c-----c-----c--a---a---t---a--tc.....
----c--a---c-c-----c-----c--a---a---t---a--tc.....
----c-----ctt-----c-----c--a---a---t---a--tc.....
----c-----c-g-----g--g-----cg-ta-t---ga-gct--aaggtagt...
----c-----g-----cc-g-----gt--gg-c-----ta--a.....

```

D87000 Homsap IGLV4-60*02 F
Y12418 Homsap IGLV2-8*03 F
M30446 Homsap IGLV1-51*02 F

---c-----c-g-----g-----cg-ta-t---ga-gct--aaggtagt...
-----c-a---c-c-----c-----c---a---a---t---ag-tc.....
-----c-----ctc-----c-----c---a---c-----aaaa.....

9
M94116 Homsap IGLV1-40*01 F
X53936 Homsap IGLV1-40*02 F
Y12415 Homsap IGLV2-11*03 F
Y12413 Homsap IGLV2-14*04 F
Z22192 Homsap IGLV1-40*03 F
AC279317 Homsap IGLV4-60*03 F
X71966 Homsap IGLV3-21*01 F
D87000 Homsap IGLV4-60*02 F
Y12418 Homsap IGLV2-8*03 F
M30446 Homsap IGLV1-51*02 F

2-IMGT _____<-----
.....tccagtttacaaagtggggtccca...tcaagattcagcggcagtgga
.....ag--a-cgg-cctca-----t...gacc-----tct---tccaag
.....ag--a-cgg-cctca-----t...gacc-----tct---tccaag
.....agt-agcgg-cctca-----t...gac-c---tct---tccaag
.....agt-a-cgg-cctca-----tt-t...aatc-c---tct---tccaag
.....ag--a-cgg-cctca-----t...gacc-----tct---tccaag
.....ggaagc-a--acaagggg--c--a--t--t...gac-c---tca---tcca-c
.....ag-gaccgg-cctca---a---t...gagc-----tct---tccaac
.....ggaagc-a--acaagggg--c--a--t--t...gac-c---tca---tcca-c
.....agt-agcgg-cctca-----t...gac-c---ttt---tccaag
.....aat-agc-g-cctca---a-t--t...gacc-----tct---tccaag

9
M94116 Homsap IGLV1-40*01 F
X53936 Homsap IGLV1-40*02 F
Y12415 Homsap IGLV2-11*03 F
Y12413 Homsap IGLV2-14*04 F
Z22192 Homsap IGLV1-40*03 F
AC279317 Homsap IGLV4-60*03 F
X71966 Homsap IGLV3-21*01 F
D87000 Homsap IGLV4-60*02 F
Y12418 Homsap IGLV2-8*03 F
M30446 Homsap IGLV1-51*02 F

----- FR3-IMGT -----
.....tctgggacagatttactctcaccatcagcagcctgcagcctgaggattttgca
.....-----c--ctcagc-t-c--gg-----ctg-g--c--g-----gag--t
.....-----c--ctcagc-t-c--gg-----ctg-g--c--g-----gag--t
.....-----c-acacggc-t-c--g-----tctg-g--c--g-----gag--t
.....-----c-acacggc-t-c--g-----tctg-g--c--g-----cgag--t
.....-----cg-ctcagc-t-c--gg-----ctg-g--c--g-----gag--t
.....-----g-t--ccg-tac-----tc--a---c---t-----gag--t
.....-----acacggc--c--g-----gg-cg-ag-c-g-----gag--c
.....-----g-t--ccg-tac-----tc--a---c---tt-----gag--t
.....-----c-acacggc-t-c--g---g--tctg-g--c--g-----gag--t
.....-----c--gtcagc--c--ggg-----c-g-a--c---a---g---cgag--c

9
M94116 Homsap IGLV1-40*01 F
X53936 Homsap IGLV1-40*02 F
Y12415 Homsap IGLV2-11*03 F
Y12413 Homsap IGLV2-14*04 F
Z22192 Homsap IGLV1-40*03 F
AC279317 Homsap IGLV4-60*03 F
X71966 Homsap IGLV3-21*01 F
D87000 Homsap IGLV4-60*02 F
Y12418 Homsap IGLV2-8*03 F
M30446 Homsap IGLV1-51*02 F

----->_____ CDR3-IMGT _____
atttactattgtcaacaggctaacagtggtcccgatcaccttcggccaaggacacgactg
ga---t--c--c--gtccta-g---cag--t--gtggt-c
ga---t--c--c--gtccta-g---cag--t--gtggt-c
ga---t--c--ctgctcata-gcag-cag-tac-cttt-
ga---t--c--cagctcata--ca--cag-agc-ctct-
ga---t--c--c--gtccta-g---cag--t--gtggt
ga---t--c---g-gacctggg-----aa-a-tca
gac--t--c-----ggt-tggg-----agtagtgatcatcc
ga---t--c---g-gacctggg-----aa-a-tca
ga---t--c--cagctcata-gcag-cag-aac-attt-
ga---t--c--cgg-acatggg-t--cag--t--gtg-tgg

9
M94116 Homsap IGLV1-40*01 F
X53936 Homsap IGLV1-40*02 F
Y12415 Homsap IGLV2-11*03 F
Y12413 Homsap IGLV2-14*04 F
Z22192 Homsap IGLV1-40*03 F
AC279317 Homsap IGLV4-60*03 F
X71966 Homsap IGLV3-21*01 F
D87000 Homsap IGLV4-60*02 F
Y12418 Homsap IGLV2-8*03 F
M30446 Homsap IGLV1-51*02 F

gagattaaacga

Fri Apr 23, 2021 23:28:28 CEST

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